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Statistical estimation of genetic parameters to study variability in okra (*Abelmoschus esculentus* (L.) Moench) for enhancement in economic and quality attributes

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Abstract

The degree of genetic variety existing in accessible germplasm determines the scope of any crop improvement. An effort was made through the present investigation to appraise the genetic parameters of variability for twenty three morphology, yield and quality parameters in diverse okra genotypes. The experiment was laid under RCBD comprising of 3 replications at Vegetable Research Farm (South Block), Department of Horticulture, Banaras Hindu University, Varanasi. The results pertinent to ANOVA justified significant differences for all the studied attributes. The study showcased that the genotypic coefficient of variation (PCV) had slightly lower magnitudes as compared to analogous values of phenotypic coefficient of variation (GCV) for various studied attributes. The range of per cent GCV varied from 2.12 to 17.72% whereas range of per cent PCV varied 2.33 to 19.56%. Moderate magnitudes were noticed for all attributes in case of both genotypic as well as phenotypic coefficient of variation. The estimates of moderate GCV and PCV % (10-20%) recorded highest in number of primary branches per plant followed by vitamin C content and fruit yield in order of merit which suggested the possibility of selection for improving these characters in segregating generations. Small differences between the magnitudes of GCV and PCV% indicated less control exerted by the environmental factors on these traits. Majority of the parameters showcased heritability (broad sense) in the higher range, whereas, low per cent of heritability was not noticed for any of the traits. The top three traits exhibiting high heritability conjoined with high genetic advance (as % of mean) included plant height followed by internode length and number of primary branches per plant which pointed out the role of more of additive gene effects, thereby suggesting that further improvement of these parameters might be efficacious through selection.

Keywords: Variability, okra, heritability, traits, genetic advance, selection

Introduction

Okra, botanically known by the name *Abelmoschus esculentus* (L) Moench, belonging to family Malvaceae and order Malvales, is often known by the name lady's finger. The commercially cultivated okra is often cross pollinated with $2n = 130$ as its somatic chromosome number, and is thought to be an amphidiploid generated by cross of *A. tuberculatus* ($2n = 58$) with a wild species ($2n = 72$). It is popularly consumed high value vegetable crop cultivated commercially for its tender pods during spring-summer and kharif seasons possessing high nutritive value and export earnings. Okra with its high moisture content is rich in vitamins and minerals and a great source of carbohydrate present in the form of mucilage. In India, okra is commercially grown and consumed round the year in multiple regions owing to the existence of varying climatic conditions prevailing in various parts of the country. Among all the states, Gujarat leads in production of okra in India followed by West Bengal and Bihar (Anonymous, 2022) ^[1]. Several favorable characteristics in okra help the plant breeders to generate quick results. The growing habits, short growing duration and broad adaptability to varying climate and soil conditions, easy emasculation, high fruit set per cent and huge quantity of seeds per fruit in okra renders feasibility for commercial exploitation of hybrid vigour.

The fulfillment of breeding objectives of a crop is correlated to the maximum existence of variability at genetic level in the population. Phenotypically diverse genotypes are most likely to generate efficient crosses. Higher genetic diversity in a population facilitates more easy fixation of traits selection (Rambabu *et al.*, 2019) ^[13].

Therefore, it is required to uncover the extent of genetic variability existing for yield and related attributes and heritability which is of immense help to the breeders to select the breeding methodologies for improvement of the particular trait. Therefore an effort was made to investigate genetic variability existing in the available okra germplasm by splitting of overall variability into its component parameters.

Materials and Methods

The present evaluation was experimented at Vegetable Research Farm (South Block), Department of Horticulture, Banaras Hindu University, Varanasi during the summer of 2020, 2021 and 2022. The experiment was designed in RBD comprising of 3 replications. The materials used for the experiment was collected from ICAR-IIVR, Varanasi which comprised of 15 diverse genotypes of okra including one check variety, belonging to different diverse morphological attributes (Table-1). Line \times Tester mating design was carried out to generate 40 F₁ crosses. Each treatment variety was sown in five rows at a distance of 60 \times 60 cm including 25 plants in a single plot. Proper package of practices that is recommended for the crop was undertaken to produce a healthy crop. Collection of data was done for the following 23 economic and quality traits [Days to 50% flowering, plant height (cm), internode length (cm), number of primary branches per plant, first flowering node, number of nodes per plant, fruit length (cm), fruit width (cm), average fruit weight (g), number of fruits per plant, fruit yield per plant (g), fruit yield (q/ha), days to first fruit picking, number of seeds per pod, seed weight per pod (g), seed yield per plant (g), seed yield (q/ha), seed index (g), TSS ($^{\circ}$ Brix), leaf chlorophyll content (spad), vitamin C content (mg/100g), crude protein content (%) and moisture content (%). The mean performances of all treatments were subjected to analysis of variance technique based on the model suggested by Panse and Sukhatme, (1984) [11]. Phenotypic and genotypic coefficient of variation has been computed according to the formulae proposed by Burton and De-Vane, (1953) [4]. Heritability in broad sense along was evaluated using the formula by stated by Hanson *et al.* (1956) [6]. The genetic advance was computed by making use of the formula stated by Johnson *et al.* (1955) [7].

Table 1: List of genotypes of okra utilized for the study

Sl. No.	Genotypes of okra	Source
Lines		
1	Kashi Mangali	ICAR- Indian Institute of Vegetable Research, Varanasi
2	Kashi Vibhuti	
3	Lam sel-1	
4	Kashi Mohini	
5	SB-6	
6	VRO-401	
7	EC-169419	
8	IC-128911	
9	IC-85595	
10	EMS-8-1	
Testers		
1	Arka Anamika	
2	Hisar Unnat	
3	Azad bhindi-2	
4	Varsha Uphar	
Commercial check- Kashi Pragati		

Results and Discussion

ANOVA was done to gauge the importance of variations among replications, genotypes, and other partitioning sources of variation. For all the traits encompassed in the experiment, differences within the genotypes were significant at 0.01 level of significance highlighting the presence of ample variation among the genotypes under study. Similar findings was given by Singh *et al.* (2007) [20]; Mazid *et al.* (2013) [10]; Sravanthi (2017) [22] and Kharat *et al.* (2022) [8].

Simple measurements of variability include the genotypic and phenotypic coefficient of variation which are frequently employed to evaluate variability. Environmental effects on the manifestation of the studied character can be shown by the fact that the estimates of PCV being larger than the analogous GCV values in case of the studied attributes. According to Sivasubramanian and Madhavamenon (1973) [21], there are broadly three sections of coefficient of variation (GCV and PCV): low (< 10%), moderate (10%–20%), and high (> 20%). The range of per cent GCV varied from 2.12 to 17.72% whereas range of per cent PCV varied 2.33 to 19.56%. For all the traits, higher estimates of phenotypic coefficient of variation was spotted as compared to their corresponding genotypic coefficient of variation. In a study by Singh *et al.* (2007) [2]; Sharma *et al.* (2012) [17]; Rekha *et al.* (2015) [16]; Sravanthi (2017) [22]; Rathod *et al.* (2019) [15]; Vani *et al.* (2021) [24]; Awasthi *et al.* (2022) [2] and Barman *et al.* (2023) [3], it was observed that for majority of traits, the PCV values were of greater estimates than that of GCV considering all the traits. For most of the traits, moderate magnitudes of genotypic and phenotypic coefficient of variation was observed. The estimates of moderate GCV and PCV % were noted in parameters *viz.*, number of primary branches per plant (17.72 and 19.56%), vitamin C content (15.48 and 16.35%), fruit yield (14.15 and 14.75%), number of seeds per pod (13.64 and 13.82%), fruit yield per plant (13.60 and 16.04%), first flowering node (13.16 and 14.97%), internode length (12.93 and 14.48%), no. of fruits per plant (11.48 and 12.25%), plant height (11.34 and 11.44%), seed yield (11.19 and 12.18%), seed yield per plant (10.89 and 11.94%), fruit width (10.11 and 12.42%) respectively, indicating greater chance of improving these characters as these characters' expressions are governed by genetic factors and are less influenced by environment. The presence of such moderate magnitudes suggest that the genetic variation in the studied population is enough to perform selection for improvement. The findings of this experiment were in agreement with similar investigations conducted by Ramgiry *et al.* (2017) [14]; Thulasiram *et al.* (2017) [23]; Rambabu *et al.* (2019) [13]; Vani *et al.* (2021) [24] and Singh *et al.* (2023) [19].

The GCV with lower magnitudes but PCV with moderate magnitudes were recorded in parameters namely seed index (9.59 and 11.22%), seed weight per pod (9.42 and 11.07%) and TSS (8.08 and 11.42%) respectively, whereas, lower magnitudes of both GCV and PCV% were noted in case of number of nodes per plant (8.75 and 9.62%), leaf chlorophyll content (8.52 and 8.93%), crude protein content (8.47 and 9.88%), days to 50% flowering (8.04 and 9.58%), days to first fruit picking (7.83 and 8.04%), average fruit weight (7.19 and 8.80%), fruit length (6.13 and 7.13%), and moisture content (2.12 and 2.34%) respectively.

Heritability is an appropriate index of transfer of character from parents to the next generation. Heritability estimates is employed for predicting genetic gain and plays crucial role to

hint the dependability of estimate of phenotypic value as a guide to estimates of genetic. It is concluded from Table. 2, that high heritability in broad sense was reported in plant height (98.32%), number of seeds per pod (97.43%), days to first fruit picking (94.64%), fruit yield (92.09%), leaf chlorophyll content (91.05%), vitamin C content (89.67%), number of fruits per plant (87.87%), seed yield (84.32%), seed yield per plant (83.16%), number of nodes per plant (82.62%), moisture content (82.17%), number of primary branches per plant (82.13%), internode length (79.79%), first flowering node (77.28%), fruit length (74.08%), crude protein content (73.62%), seed index (72.99%), seed weight per pod (72.45%), fruit yield per plant (71.88%) and days to 50% flowering (70.46%) for genotypes including parents and hybrids. The genetic advance is a standard index of the progress that could be achieved as a result of selecting most suitable genotypes. High genetic advance as percentage of mean shows maximum control of attributes through action of additive gene effects and thereby effective improvement of this trait at genetic level is feasible through proper selection. Moderate GAM explained that average role of both additive and non-additive genes on the expression of these characters.

It was observed that genetic advance as per cent of mean (GAM) was found highest for number of primary branches per plant (33.09%) followed by vitamin C content (30.19%), fruit yield (27.98%) in order of merit.

The present experiment demonstrated high heritability conjoined with high genetic advance as percentage of mean for traits viz., plant height, followed by internode length, number of primary branches per plant, first flowering node, number of fruits per plant, fruit yield per plant, fruit yield, number of seeds per pod, seed yield per plant, seed yield and vitamin C content indicating that the direct selection may be advantageous as high heritability along with high genetic advance estimates suggest dominating aspect of additive gene effect and less interference of environment for these characters. Heritability along with GAM values are helpful in predicting the genetic progress that might be officiously achieved through proper trait selection. These findings on presence of genetic variation of traits in okra were in agreements with experiments by Singh *et al.* (2006)¹⁸; Prakash *et al.* (2011)¹¹²; Mazid *et al.* (2013)¹¹⁰; Rekha *et al.* (2015)¹¹⁶; Chandramouli *et al.* (2016)¹⁵ and Kumar *et al.* (2021)¹⁹.

Table. 2: Assessment of range, mean and genetic parameters of variation for 23 attributes in okra

Characters	Range		Mean	G.C.V (%)	P.C.V (%)	Heritability (broad sense) (%)	Genetic Advance as % mean
	Min.	Max.					
Days to 50% flowering	37.00	51.33	44.82	8.15	9.68	70.79	14.12
Plant height (cm)	70.00	134.00	112.90	11.33	11.44	98.15	23.13
Internode length (cm)	4.22	7.04	5.54	12.94	14.48	79.79	23.81
Number of primary branches per plant	2.07	4.28	3.38	17.72	19.56	82.13	33.09
First flowering Node	4.45	8.07	6.42	13.16	14.97	77.28	23.83
Number of nodes per plant	18.75	26.82	23.18	8.75	9.62	82.62	16.38
Fruit length (cm)	9.31	12.34	11.24	6.13	7.13	74.09	10.88
Fruit width (cm)	1.04	1.79	1.41	10.11	12.42	66.25	16.95
Average fruit weight (g)	11.72	16.89	14.86	7.19	8.80	66.78	12.11
Number of fruits per plant	16.27	25.75	21.61	11.48	12.25	87.87	22.17
Fruit yield per plant (g)	235.51	390.40	321.59	13.59	16.04	71.88	23.75
Fruit yield (q/ha)	66.59	108.69	88.92	14.15	14.75	92.09	27.98
Days to first picking	45.09	61.65	51.94	7.86	8.04	94.64	15.68
Number of seeds per pod	38.60	63.88	53.51	13.65	13.82	97.43	27.74
Seed weight per pod (g)	2.54	4.17	3.51	9.42	11.06	72.45	16.52
Seed yield per plant (g)	50.34	84.38	74.14	10.88	11.94	83.16	20.45
Seed yield (q/ha)	12.50	23.18	20.46	11.19	12.18	84.32	21.16
Seed Index (g)	5.09	7.44	6.57	9.59	11.22	72.99	16.87
TSS (°Brix)	2.57	4.13	3.59	8.08	11.42	50.05	11.77
Leaf chlorophyll content (nmol/cm ²)	50.34	72.73	63.05	8.52	8.92	91.05	16.74
Vitamin C content (mg/100g)	13.06	25.29	19.82	15.48	16.35	89.67	30.19
Protein content (%)	9.83	15.23	13.53	8.47	9.88	73.62	14.98
Moisture content (%)	82.58	90.25	86.97	2.12	2.33	82.17	3.95

Conclusion

The outcome of analysis from present examination of genetic parameters clearly specify that greater variability exist amidst all the traits of the studied genotypes. The PCV had a similar trend but slightly higher to corresponding GCV for all the attributes. Number of primary branches per plant had the highest GCV as well as PCV values, whereas moisture content had the lowest. All the traits including quantitative and qualitative characters were found with high per cent of broad sense heritability. The top traits revealing high heritability and high genetic advance were plant height, followed by internode length and number of primary branches per plant merit wise. This highly indicated the salient action of additive gene effects for these parameters.

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